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"Cloning, Sequencian and Express.",
Streptococcus uberis.",
Submitted (ACG 1995) - Fil. 1001.
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Patent No. 5863543
SEMEPAL INFORMATION:
                                                                                                                                                                                                                                                               Zip: 94301
"CMPUTER PEADABLE FORM:
MEDICM TYPE: Floppy disk
"OMPOTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prod. Not is the number of results gredithed by chance to have a score greater than or equal to the score of the result being printed, and is derived by unifying finite time.
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547.719 Million cell updates/sec
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Japop 19.6 , Gapext 0.5
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256 2 US-08-658-277-3
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Patent No. 5863543
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Best Local Similarity

Matches 228; Conservation
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D.
SOFTWARE: PATENTIN BALLSON BL., VHICH BL
CURRENT APPLICATION LACA
APPLICATION NUMBER: B. J. J.
FILING DATE: B. J. J. J.
CLASSIFICATION: 53/
AUTORNEY/AGENT INFORMATION:
PEGIOSPATION MUMBER: B. J. J.
PEGEOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COMPOTER READABLE HORM:

MEDIUM TYPE: FLORTY 1158

COMPOTER: IRM PT TOTALLIO
COPERATING SYSTEM: FLORTY 1150

SOFTWARE: PATENTION FAIL AND RELIGIOUS FLORTY

APPLICATION DATA

APPLICATION DATA

APPLICATION DATA

CLASSIFICATION SOFT

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REGISTRATION NUMBER: 11.18

REGISTRATION NUMBER: 1
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APPLICANT: 31449, M.1
APPLICANT: Potter, ACTION A
APPLICANT: MacLachian, Entire
TITLE OF INVENTION. "ACTION IN THE
NUMBER OF SEQUENCES: 4
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ADDRESSE: Reed & Piling Ci
STREET: 285 Hamilton Associat, Suite 20
CITY: Palo Alto
STATE: California
COUNTRY: USA
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Past processing: Minimum Match 90% Maximum Mitch 190%
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Perfect score:
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BLOSUM62
Gapop 10.3 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                          118974 seqs, 19401057 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  January 11, 2003, 18:57:40 /
                                                                                                                                                                                                                                                                                                                                                                                      US-09-234-733K-5
1118
1 MQ1WF1P-MMESHUTO1FF
                                                                                                                                                                                                             Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by amilyots of the total score distribution.

### SUMMARIES

Preult Query No. South Marub Length DB ID

Description

Search completed: January 13, 2003, 16:00:38 Job time: 8.00826 secs

No matches found

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GenCore version 5.1.3 Compugen Dtd.
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"M protein - protein search, using sw model

January 12, 2003, 15-56-17 ; Search Fime 12-612 Seconds - without alignments) 1604-450 Million cell updates/sec

Title: Perfect score: US-09 244-733A-5 1118 1 MGIMMOQPONMBOMMIOQRE..... ....VAQMOQEIRMLQEMLNTALQ DD8

Shoring table:

BLGSUMK2 Gapop 10.0 , Gapext 6.5

Searched:

Total number of hits satisfying chosen parameters:

283224 segs, 36134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000 ເພີ່ມເປດ

Post-processing: Minimum March 90% Maximum March 100% Listing first 45 summaries

Database : PIR 73: \*
1: pir1: \*
2: pir2: \*
3: pir3: \*
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by inityets if the tital score distribution.

# SUMMARIES

Result Query
No. Score Match Length DB ID

Description

No matches found

Search completed: January 13, 2003, 15:59:41 Job time : 13.6612 secs

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GenCore version 5.1.3 Compugen Ltd.
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(M protein - protein search, using sw model

B.H. 011: January 19, 2003, 15-53-32, Search time 4 00326 Seconds (without alignments) 1180 855 Million cell updates/sec

Title: Perfect sgore:

US-09-234-733A-5 1318 1 NQINVO(FÖMMBOMVIS,WE .... VAÇVEÇETKYEÇERLNTALÇ 228

Society table:

Searched: 112892 segs, 41476328 residues BLOSUM62 Gapop 10.0 , dapext 0.5

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 MAXIMUM DB seq length: 260vouve00

Post processing: Minimum Match 90% Maximum Match 190% Listing Eirst 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the rotal score distribution.

SUMMARIES

Pesul: Query
No. Score Match Length DB ID

Description

No matches found

Search completed: January 13, 2003, 15:58:05

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Post-processing: Minimum Match 90% Maximum Mar h 100
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## SUMMARIES

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Post processing: Minimum Match 90%
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US-98-658-277-2
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Patent No. 5863543
GENERAL INFORMATION:
Zip: 94301
COMPUTER READABLE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                    APPLICANT: Jiang, Min
APPLICANT: Forter, Andrew A.
APPLICANT: MacLachian, Philip R.
TITLE OF INVENTIAL. TAMP FACTOR OF STREPTOCOCCUS CHERIS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                           ADDRESSE: Peed & Public LLP
STREET 1285 Hamilton Avenue, Suite 100
CITY. Palo Alto
STATE California
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Score Match Length DB ID
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TOPOLOGY: iinea;
MOLECCLE TYPE: pro's::
US-08-658-277-2
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MEDIUM TYPE PIGHTY THEN
COMPUTER: IBM PC COMPUTER:
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STREET: Paid Alto
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ATTORNEY/AGENT INFIFMATE N
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Result Query
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Perfect score.
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2: /cqn2-6/prodata/i/pubga/pot NEW FUB.pep:*

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10: /iji /cj. data/i/pubga/pot NEW FUB pep:*

10: /iji /cj. data/i/pubga/pot NEW FUB pep:*

11: /iji /cj. data/i/pubga/pot NEW FUB pep:*

12: /iji /cj. data/i/pubga/pot NEW FUB pep:*

13: /cj. data/i/pubga/pot NEW FUB pep:*

14: /cj. data/i/pubga/pot NEW FUB pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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1252
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                                                                                                                                                                                   SUMMARIES
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Search completed: January 13, 2003, 16:00:38

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Title:
Perfect score:
Sequence:
                                        Result Query
No. Score March Length DB ID
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Maximum DB seq length: 20shdddddo
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Maximum Match 100%
Disting first 45 summaries
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No matches found
                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a space greater than or egoal to the score of the result being printed, and is derived by analysis of the form! shore distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 13.7 , Gapext 0.8
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1252
1 MBEKKLIYLT3SIANITLES......VAQVDQBIKVLQBALNTALQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 17, 2003, 18,86 10 , Search time 15,3388 Seconds (without alignments)
1624.450 Million cell updates/sec
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                                                          Description
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Search completed: January 13, 2003, 15:59:41
Joh time : 16.3388 secs

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Fun on:
                                           CM protein - protein search, using sw model
Copyright (c) 1993 - 2003 Compugen Ltd.
```

Parfect score: US-69-244-733A 2 1252

1 MEFERHLYLFGSIAGIILrs.....VAÇVUÇEIKVLÇENJNIALQ 256

Scoring table: BLOSUM62 Japop 10:0 , Gapext 0.5

112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters:

0

Minimum IB seq length: % Maximum IB seq length: 2000000000

East-processing: Minimum Match 90% Maximum Match 190% Disting first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chappe to have a score greater than or equal to the score of the result being printed, and in derived by analytic of the total coore distribution.

SUMMARIES

Result Query No. Score Match Length DB ID

Description

No matches found